

1/26

TWIK 2

Input file FthKa020g04.seq; Output File FthKa020g04.tra
Sequence length 3452

M V D R G P L L T S A I I I F Y L A
TCGGGAGGCC ATG GTG GAC CGG GGC CCT CTG CTC ACC TCG GCC ATC ATC TTC TAC CTG GCC
I G A A I F E V L E E P H W K E A K K N
ATC GGG GCG GCG ATC TTC GAA GTG CTG GAG GAG CCA CAC TGG AAG GAG GCC AAG AAA AAC
Y Y T Q K L H L L K E F P C L G Q E G L
TAC TAC ACA CAG AAG CTG CAT CTG CTC AAG GAG TTC CCG TGC CTG GGT CAG GAG GGC CTG
D K I L E V V S D A A G Q G V A I T G N
GAC AAG ATC CTA GAG GTG GTA TCT GAT GCT GCA GGA CAG GGT GTG GCC ATC ACA GGG AAC
Q T F N N W N W P N A M I F A A T V I T
CAG ACC TTC AAC AAC TGG AAC TGG CCC AAT GCA ATG ATT TTT GCA GCG ACC GTC ATT ACC
T I G Y G N V A P K T P A G R L F C V F
ACC ATT GGA TAT GGC AAT GTG GCT CCC AAG ACC CCC GCC GGT CGC CTC TTC TGT GTT TTC
Y G L F G V P L C L T W I S A L G K F F
TAT GGT CTC TTC GGG GTG CCG CTC TGC CTG ACG TGG ATC AGT GCC CTG GGC AAG TTC TTC
G G R A K R L G Q F L T K R G V S L R K
GGG GGA CGT GCC AAG AGA CTA GGG CAG TTC CTT ACC AAG AGA GGT GTG AGT CTG CGG AAG
A Q I T C T V I F I V W G V L V H L V I
GCG CAG ATC ACG TGC ACA GTC ATC TTC ATC GTG TGG GGC GTC CTA GTC CAC CTG GTG ATC
P P F V F M V T E G W N Y I E G L Y Y S
CCA CCC TTC GTA TTC ATG GTG ACT GAG GGG TGG AAC TAC ATC GAG GGC CTC TAC TAC TCC
F I T I S T I G F G D F V A G V N P S A
TTC ATC ACC ATC TCC ACC ATC GGC TTC GGT GAC TTT GTG GCC GGT GTG AAC CCC AGC GCC
N Y H A L Y R Y F V E L W I Y L G L A W
AAC TAC CAC GCC CTG TAC CGC TAC TTC GTG GAG CTC TGG ATC TAC TTG GGG CTG GCC TGG
L S L F V N W K V S M F V E V H K A I K
CTG TCC CTT TTT GTC AAC TGG AAG GTG AGC ATG TTT GTG GAA GTC CAC AAA GCC ATT AAG
K R R R R R K E S F E S S P H S R K A L
AAG CGG CGG CGG CGA CGG AAG GAG TCC TTT GAG AGC TCC CCA CAC TCC CGG AAG GCC CTG
Q V K G S T A S K D V N I F S F L S K K
CAG GTG AAG GGG AGC ACA GCC TCC AAG GAC GTC AAC ATC TTC AGC TTT CTT TCC AAG AAG
E E T Y N D L I K Q I G K K A M K T S G
GAA GAG ACC TAC AAC GAC CTC ATC AAG CAG ATC GGG AAG AAG GCC ATG AAG ACA AGC GGG
G G E T G P G P G L G P Q G G G L P A L
GGT GGG GAG ACG GGC CCG GGC CCA GGG CTG GGG CCT CAA GGC GGT GGG CTC CCA GCA CTG
P P S L V P L V V Y S K N R V P T L E E
CCC CCT TCC TCC CTG GTG CCC CTG GTA GTC TAC TCC AAG AAC CGG GTG CCC ACC TTG GAA GAG
V S Q T L R S K G H V S R S P D E E A V
GTG TCA CAG ACA CTG AGG AGC AAA GGC CAC GTA TCA AGG TCC CCA GAT GAG GAG GCT GTG
A R A P E D S S P A P E V F M N Q L D R
GCA CGG GCC CCT GAA GAC AGC TCC CCT GCC CCC GAG GTG TTC ATG AAC CAG CTG GAC CGC
I S E E C E P W D A Q D Y H P L I F Q D
ATC AGC GAG GAA TGC GAG CCA TGG GAC GCC CAG GAC TAC CAC CCA CTC ATC TTC CAG GAC
A S I T F V N T E A G L S D E E T S K S
GCC AGC ATC ACC TTC GTG AAC ACG GAG GCT GGC CTC TCA GAC GAG GAG ACC TCC AAG TCC
S L E D N L A G E E S P Q Q G A E A K A
TCG CTA GAG GAC AAC TTG GCA GGG GAG AGC CCC CAG CAG GGG GCT GAA GCC AAG GCG

Fig. 1

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P L N M G E F P S S S E S T F T S T E S
CCC CTG AAC ATG GGC GAG TTC CCC TCC TCC GAG TCC ACC TTC ACC AGC ACT GAG TCT
E L S V P Y E Q L M N E Y N K A N S P K
GAG CTC TCT GTG CCT TAC GAA CAG CTG ATG AAT GAG TAC AAC AAG GCT AAC AGC CCC AAG
G T *
GGC ACA TGA

GGCAGGGCCGGCTCCCCACCCCACCTTGATGGCTCTTCCCCCTCACCCCTAGGGTGTCCAAGATGACCAGGACGCC
TGGCCCTGGTGGGGGGCAGCCTCGGAACCTGGAGTGGGGCCAGGGCCTTCATAACCTCCATCATCCTCAGCTA
GATGTATGCCGGACAGGGCTCTGTTCTCAGCTAACCTGGCTGTGGGCATCTGTCCTGAGCTTGGCT
GGTGTATCTACAATGCAAAGACATGCTGGCTGGCGGACAGGTGGCAGGACTGACCC TGAGGAGGCCTGCCTGCAG
GGTCTTGTCTCACCAATTGGTGGAGTATCACACGGTCTCTGAGGTCTGGGCCTCAGCTGTTAAGTTACCGGTAT
TACTGAGCTCGGCATTGGAGAGGGAGCTCTGAAGTGTCTGGGAGGTACCGCTGTGCGTGGGTCAAGGTGTTCCGTA
CCACAGCAGGAGCAGGGCTGCCGCATCCAGCTGGGCTGCCGGTCAGGTGGCACCTACTACAAACCGTAGTG
GGTGGAGGCTGCTGGAGGTGGAGTGAGGAGATGAGGGCAGGGCTCAAACAGTCCTGACTCACAGGGCTGGAAACA
AGTCCTATGTGGCCTGGGCCTGGGTCTCATCCCTTGTTGCTACTCAGGCCAGCCCAGAGCTGTGTTCCCT
GTCTCAGGTCAAGCAGTGGCAGACGCAAGGCTTCTGTGGGCCCTGGGCTGGGTCAAGTCCTGACTCACAGGGCTGGAAACA
TACTGGAAGCCGGACTGCTAGGGCTGGTGGCCAGGGAGCTGCAAGAGTGAGGCTCAGCTCTGGCTGGTCTGCCCTTA
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TCCCTGTGCCCTGAACAAGGACCTCACTGCCGCTCCCCCTCCACCAAGCCCCCTGGCCAGGCAGGGTGAGGCCAA
ATTGCTCTGGCCCACAAATGGGTGATGGTCAGATATGTGAATCAAGCTCCTTCTAGCTAGTGTGTTGATGTGACG
TGTGTGTCACAGTGCCTGTCACACGACACCTGTGCACTCGTGTGTTAAGAAAGGAAAGGATTGGCTGG
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ACTGCTGTTTATATACCTGGAATCTGTTGGCTCAGAGCCAGTGGTAAAGAGCAGGGTCCAAGGATTGGGAG
ATCTAGTGTCTGCCCTGCCCTGCAACTCAATTGGCCTTTGCGTACCTCATCCAAGGCCATGATGTCAAGGGC
CATGTCCCCAAGCAGAGGTGGAGAAGGGGACACTGAGGTGAGCAAAAGCAGGAAGGGCATCCACTGCCGGTGACTGGA

Fig. 1 (continued)

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES

**Title: NOVEMBER 2010 CHARTER MILESTONES AND 2011
THEREFOR**

new/Agent::k

Attorney/Agent: Kerri Pollard Schray
KERRI POLLARD SCHRAY PLLC

Docket No.: MPI99-025CP2DV1M

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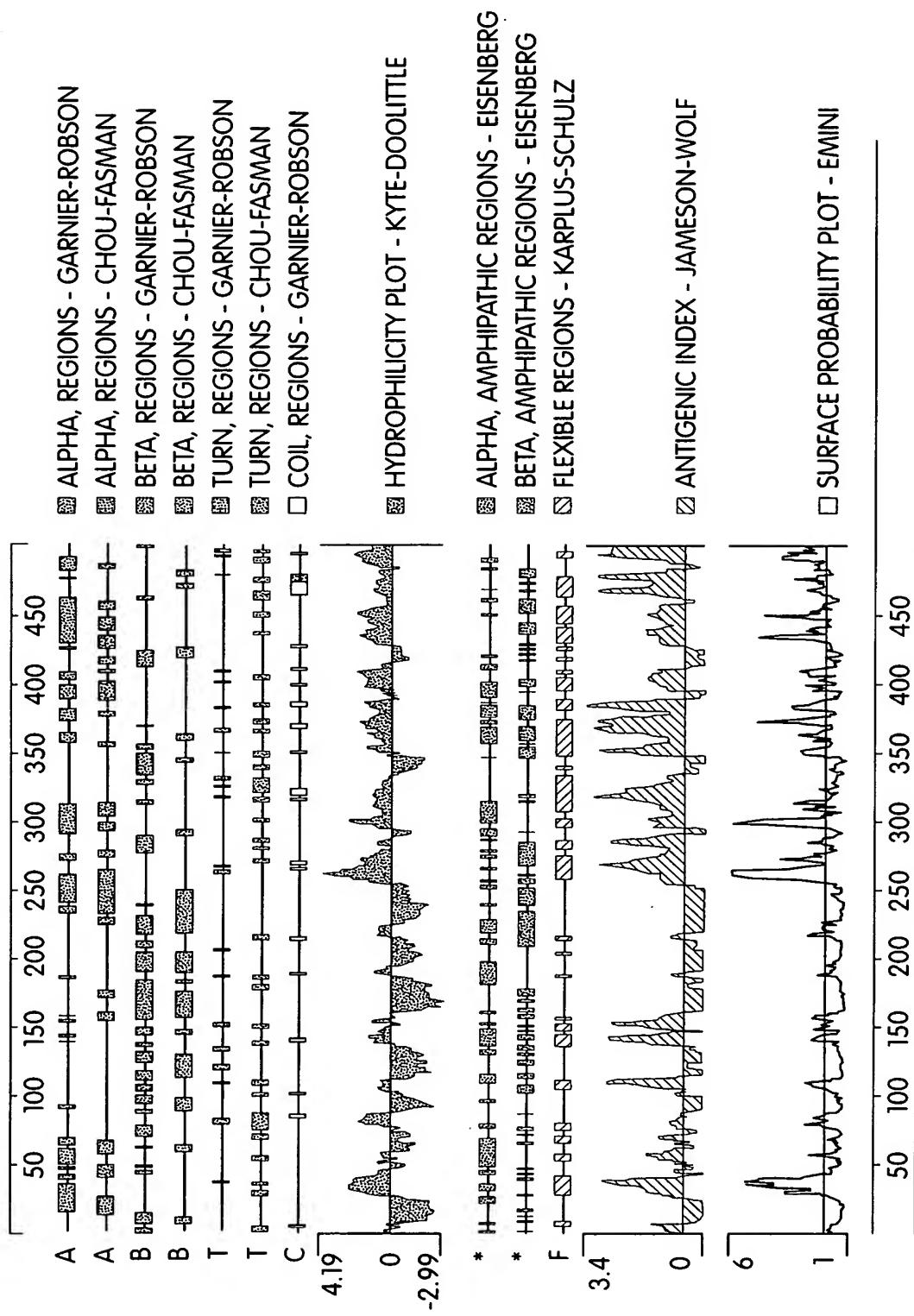


Fig. 2

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Input file Athua133f10.seq; Output File Athua133f10.tra
Sequence length 1575

CAACCGCTCCGCCGGCACCAGCAGGCAGGAGAGATACGAGCTGGACGCCCTCCCTCCCACCGGGT
M Y R P R A R A A
CCTAGTCCACCGCTCCGGCGCCGGCTCCCGCTCTCCGCT ATG TAC CGA CCG CGA GCC CGG GCG GCT
P E G R V R G C A V P G T V L L L L A Y
CCC GAG GGC AGG GTC CGG GGC TGC GCG GTG CCC GGC ACC GTG CTC CTG CTG CTC GCC TAC
L A Y L A L G T G V F W T L E G R A A Q
CTG GCT TAC CTG GCG CTG GGC ACC GGC GTG TTC TGG ACG CTG GAG GGC CGC GCG GCG CAG
D S S R S F Q R D K W E L L Q N F T C L
GAC TCC AGC CGC AGC TTC CAG CGC GAC AAG TGG GAG CTG TTG CAG AAC TTC ACG TGT CTG
D R P A L D S L I R D V V Q A Y K N G A
GAC CGC CCG GCG CTG GAC TCG CTG ATC CGG GAT GTC GTC CAA GCA TAC AAA AAC GGA GCC
S L L S N T T S M G R W E L V G S F F F
AGC CTC CTC AGC AAC ACC ACC AGC ATG GGG CGC TGG GAG CTC GTG GGC TCC TTC TTC TTT
S V S T I T T I G Y G N L S P N T M A A
TCT GTG TCC ACC ATC ACC ACC ATT GGC TAT GGC AAC CTG AGC CCC AAC ACG ATG GCT GCC
R L F C I F F A L V G I P L N L V V L N
CGC CTC TTC TGC ATC TTC TTT GCC CTT GTG GGG ATC CCA CTC AAC CTC GTG GTG CTC AAC
R L G H L M Q Q G V N H W A S R L G G T
CGA CTG GGG CAT CTC ATG CAG CAG GGA GTA AAC CAC TGG GCC AGC AGG CTG GGG GGC ACC
W Q D P D K A R W L A G S G A L L S G L
TGG CAG GAT CCT GAC AAG GCG CGG TGG CTG GCG GGC TCT GGC GCC CTC CTC TCG GGC CTC
L L F L L P P L L F S H M E G W S Y T
CTG CTC TTC CTG CTG CTG CCA CCG CTG CTC TTC TCC CAC ATG GAG GGC TGG AGC TAC ACA
E G F Y F A F I T L S T V G F G D Y V I
GAG GGC TTC TAC TTC GCC TTC ATC ACC CTC AGC ACC GTG GGC TTC GGC GAC TAC GTG ATT
G M N P S Q R Y P L W Y K N M V S L W I
GGA ATG AAC CCC TCC CAG AGG TAC CCA CTG TGG TAC AAG AAC ATG GTG TCC CTG TGG ATC
L F G M A W L A L I I K L I L S Q L E T
CTC TTT GGG ATG GCA TGG CTG GCC TTG ATC ATC AAA CTC ATC CTC TCC CAG CTG GAG ACG
P G R V C S C C H H S S K E D F K S Q S
CCA GGG AGG GTA TGT TCC TGC TGC CAC CAC AGC TCT AAG GAA GAC TTC AAG TCC CAA AGC
W R Q G P D R E P E S H S P Q Q G C Y P
TGG AGA CAG GGA CCT GAC CGG GAG CCA GAG TCC CAC TCC CCA CAG CAA GGA TGC TAT CCA
E G P M G I I Q H L E P S A H A A G C G
GAG GGA CCC ATG GGA ATC ATA CAG CAT CTG GAA CCT TCT GCT CAC GCT GCA GGC TGT GGC
K D S *
AAG GAC AGC TAG
TTATACTCCATTCTTGGTCGTCTCGGTAGCAAGACCCCTGATTTAAGCTTGCACATGTCCACCCAAACTAAA
GAATCACATTTCCATCCACCCTAGAGGCTGGGTGCAAGCTATGATTAATTCTGCCAATAGGGTATACAGAGACATGT
CCTGGGTGACATGGATGTGACTTCTGGGTGTCGGGGCAGCATGCCCTCTCCCCACTTCCTTACTTAGGGCTGC
AATGCCGCCATATGATGGCTGGGAGCTGGCAGCCATACGGCACCATGAAGTAGCGGCAATGTTGAGCGGCACAAT
AAGATAGGAAGAGTCTGGATCTGTGATGATCACAGAGCCATCTAACAAACGGAATATCACCCGACCTCCTTATGTGA
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Fig. 3

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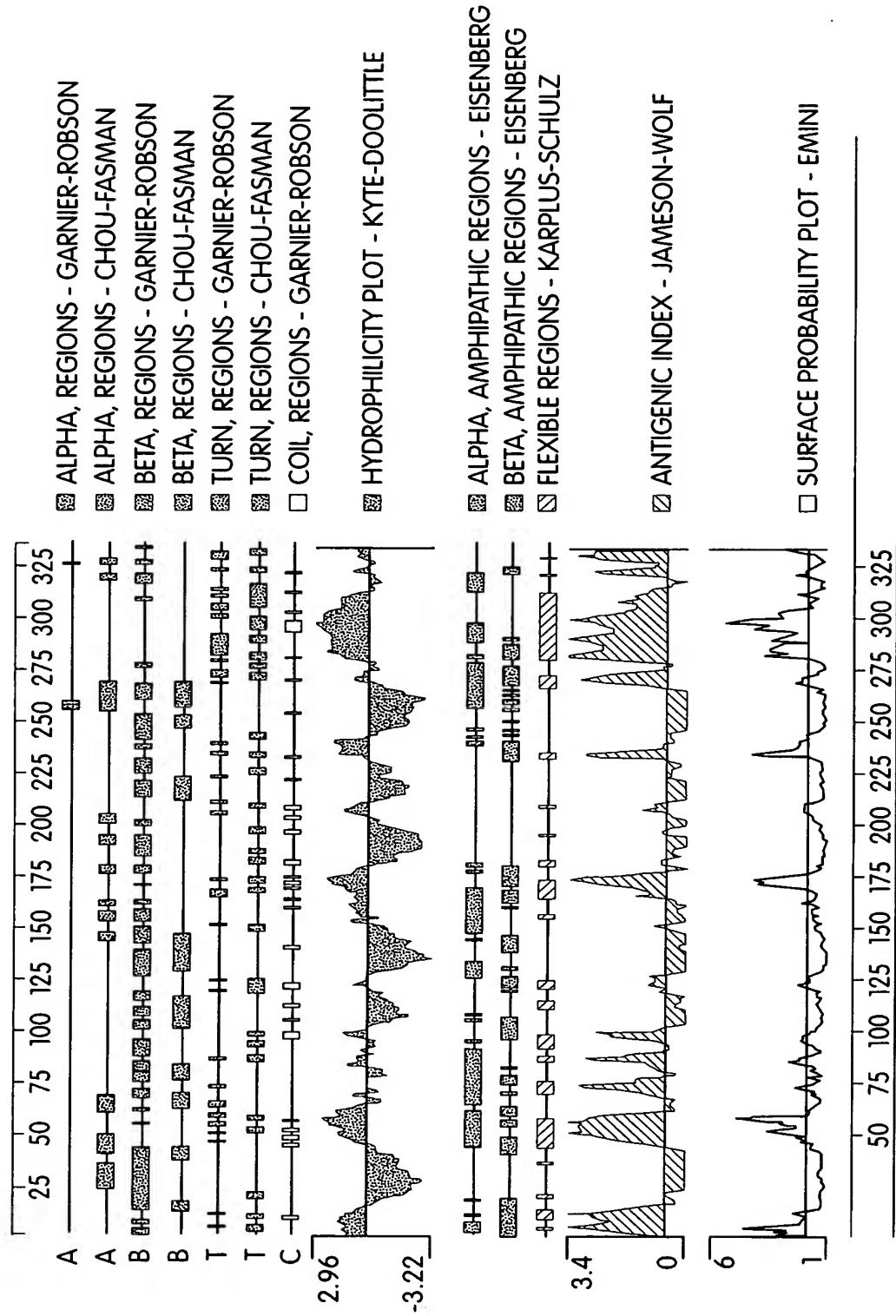


Fig. 4

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TWIK 4

Input file AthTb005e07.seq; Output File AthTb005e07.tra

Sequence length 2287

TAAAAAGCTGCGGAATTCTAATATCACTCACTATAGGGAGTCGACCCACGCCGTCCGGAACTAGGTGCCAGACGGTCCGG
M R R G A
AGGCAGGGGCCACGTCAGCAGGGGCCACCCAGGGCTCGCGGGTCCCGGTGGTGCC ATG CGG AGG GGC GCG
L L A G A L A A Y A A Y L V L G A L L V
CTT CTG GCG GGC GCC TTG GCC GCG TAC GCC GCG TAC CTG GTG CTG GGC GCG CTG TTG GTG
A R L E G P H E A R L R A E L E T L R A
GCG CGG CTG GAG GGG CCG CAC GAA GCC AGG CTC CGA GCC GAG CTG GAG ACG CTG CGG GCG
Q L L Q R S P C V A A P A L D A F V E R
CAG CTG CTT CAG CGC AGC CCG TGT GTG GCT GCC CCC GCC CTG GAC GCC TTC GTG GAG CGA
V L A A G R L G R V V L A N A S G S A N
GTG CTG GCG GCC GGA CGG CTG GGG CGG GTC GTG CTT GCT AAC GCT TCG GGG TCC GCC AAC
A S D P A W D F A S A L F F A S T L I T
GCC TCG GAC CCC GCC TGG GAC TTC GCC TCT GCT CTC TTC GCC AGC ACG CTG ATC ACC
T V G Y G Y T T P L T D A G K A F S I A
ACC GTG GGC TAT GGG TAC ACA ACG CCA CTG ACT GAT GCG GGC AAG GCC TTC TCC ATC GCC
F A L L G V P T T M L L L T A S A Q R L
TTT GCG CTC CTG GGC GTG CCG ACC ACC ATG CTG CTG CTG ACC GCC TCA GCC CAG CGC CTG
S L L L T H V P L S W L S M R W G W D P
TCA CTG CTG CTG ACT CAC GTG CCC CTG TCT TGG CTG AGC ATG CGT TGG GGC TGG GAC CCC
R R A A C W H L V A L L G V V V T V C F
CGG CGG GCG GCC TGC TGG CAC TTG GTG GCC CTG TTG GGG GTC GTA GTG ACC GTC TGC TTT
L V P A V I F A H L E E A W S F L D A F
CTG GTG CCG GCT GTG ATC TTT GCC CAC CTC GAG GAG GCC TGG AGC TTC TTG GAT GCC TTC
Y F C F I S L S T I G L G D Y V P G E A
TAC TTC TGC TTT ATC TCT CTG TCC ACC ATC GGC CTG GGC GAC TAC GTG CCC GGG GAG GCC
P G Q P Y R A L Y K V L V T V Y L F L G
CCT GGC CAG CCC TAC CGG GCC CTC TAC AAG GTG CTG GTC ACA GTC TAC CTC TTC CTG GGC
L V A M V L V L Q T F R H V S D L H G L
CTG GTG GCC ATG GTG CTG GTG CTG CAG ACC TTC CGC CAC GTG TCC GAC CTC CAC GGC CTC
T E L I L L P P P C P A S F N A D E D D
ACG GAG CTC ATC CTG CTG CCC CCT CCG TGC CCT GCC AGT TTC AAT GCG GAT GAG GAC GAT
R V D I L G P Q P E S H Q Q L S A S S H
CGG GTG GAC ATC CTG GGC CCC CAG CCG GAG TCG CAC CAG CAA CTC TCT GCC AGC TCC CAC
T D Y A S I P R
ACC GAC TAC GCT TCC ATC CCC AGG
TAGCTGGGGCAGCCTCTGCCAGGCTTGGGTGTGCCCTGGCTGGACTGAGGGTCCAGGCACAGAGCTGGCTGTACA
GGAATGTCCACGAGCACAGCAGGTGATCTTGAGGCCTGCCGTCCACCGTCTCTCCTTGTTCCAGCATCTGGCTGG
GATGTGAAGGGCAGCACTCCCTGTCCCCATGTCCCCGGCTCCACTGGGCACCAACATAACCTGTTCTGTCCCTTCT

Fig. 5

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CTCATCCTCTTACACTGTGCTCTGGCTCTGGCATTCTCGCTGCCCTGTCTTCCCTTGCTGTCCTGGTT
CTCATTCTCTTCATGTTCCGKCTGKTCTCAATTAAACCACCGTCAACTGCTGATTCTACTGGGCTGTGGGCTCAG
ACCTCATTTCAGGCACCAAGATTGGTCGCTACACCCCTGGACAAGTGACTGCCGTCTGAGCCTTGATTCCCTCAGCTG
CCAAATGGGAAGAATAGAAGAATTGCCCTAAACCCCTCTGTGTGCTGGCCCTGTGCTAGACAGTGCTGGAGACATA
GTTGGGGGTGGAGAAGTGCCTTATGGAGCTTGCACTGAGGTGGACAGACCTGCCCCAGACAGTGATGCCCA
AAATGGTCAGGACTTAATGGAGGARGTGAAGGTGTTAAAGCACAGGCAGAGTGGGTAGGKCTTGAAGTCGKAGAAG
CATARGGVCTAGGCCAATCCANGCTGGAAAAGTMMGGGAGNGACNTCCTAGAGGAACGGGACATGAACTAAAGA
CCTGAANCTATGAGAAATAGGCAGGAAGAAGTTGACCTGACTCATTTTTTCAGGTGTCTCAGGGAGCAGGACCCA
TGGAGGGACCCCTGGTGTAGGCHTGGCAGATAGACTCTTCACTCAGCAGCCTGGCAGGCAGGAARCAWGWCATAGGMCC
CCAGCCCAGATYTGAATGGCMYSGGAGGTGCTGCCCTWCCRTGACACCATTGWAAGWGCTGYCCACATWTGTATGKT
GTGCCCTGGAANTCAGCCAGGTTGAGCTCAAATCCAACCTAGCCASGTCTGGCCTGTGTCCTGGGAGTCACACTAC
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Fig. 5 (continued)

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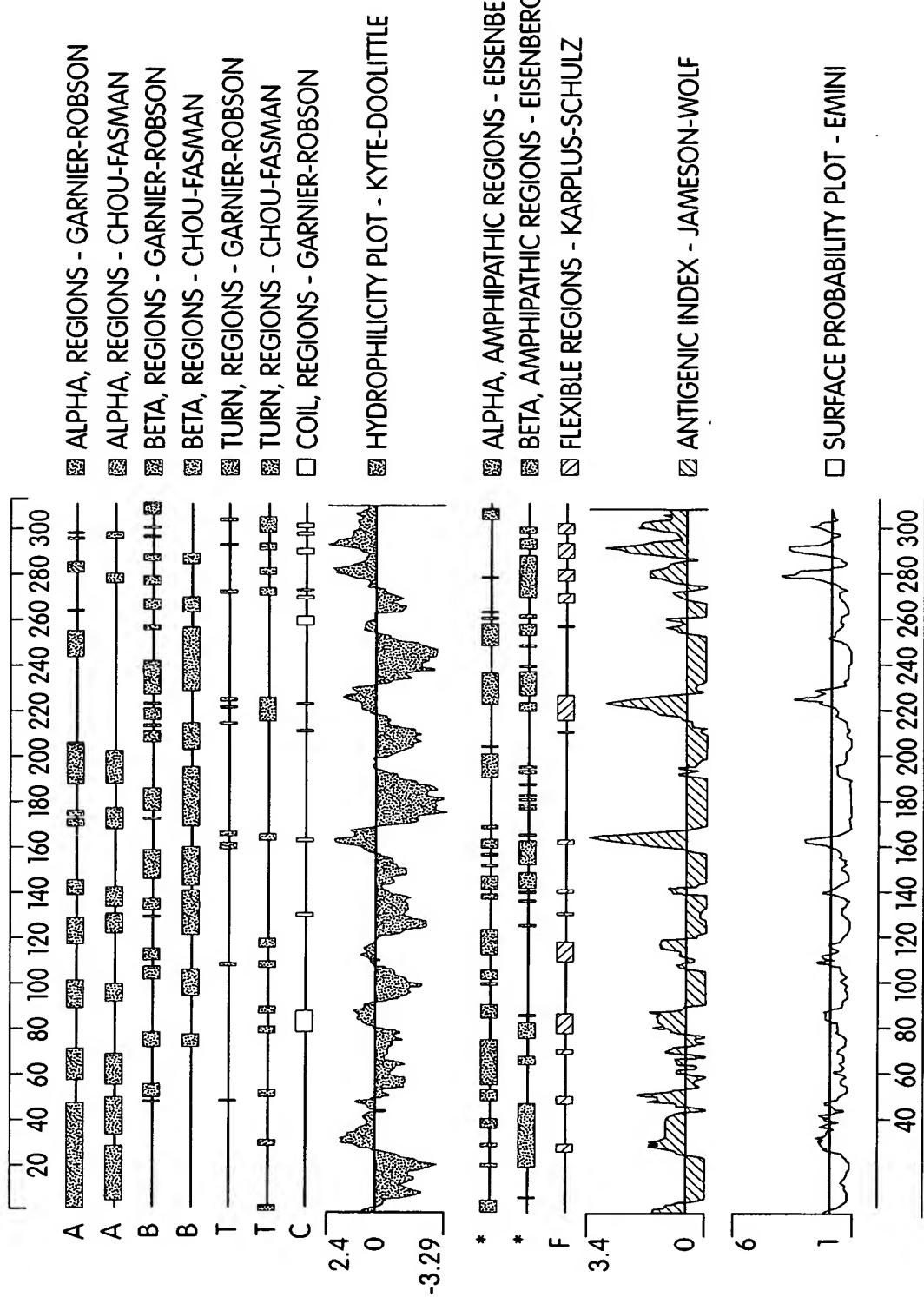


Fig. 6

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DV1M

Sheet 9 of 26

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Clustal W (1.74) multiple sequence alignment

| | | |
|-------------|--|---------|
| AthTb005e07 | MRRGALLAGALAA | YAYLVL |
| hTWIK-1 | MLQSLAGSSCVRLVERHRSAWCFGFLVLG | YLLYLVF |
| mTRAAK | MRSTTLLALLAL | VLLYLVS |
| mTREK-1 | MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII | |
| Athua133f10 | MYRPRARAAPEGRVRGCAVPGTVLLLAY | LAYLAL |
| FthKa20g4 | MVDRGPLLTSAIIF | YLAI |
| hTASK | MKRQNVRTLALIVC | TFTYLLV |

| | |
|-------------|--|
| AthTb005e07 | GALLVARLEGPHEARLRAELETLRQALLQRSPCVAAPALDAFVERVLAAGRLGRVVLANA |
| hTWIK-1 | GAVVFSSVELPYEDLLRQELRKLRKRRFLEECLSEQQLEQFLGRVLEASNYGVSVLSNA |
| mTRAAK | GALVFQALEQPHEQQAQKMDHGRDQFLRDHPVCVSQKSLEDFIGKLLVEALGGGANPETS |
| mTREK-1 | GAAVFKALEQPQEISQRTITIVIQQTFFIAQHQACVNSTELDELIQIVAAINAGIPLGNS |
| Athua133f10 | GTGVFWTLEGRAAQDSSRSFQRDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNT |
| FthKa20g4 | GAAIFEVLEEPHWKEAKNNYYTQKLHLLEKFPCLGQEGLDKILEVVSDAAGQGVAITGNQ |
| hTASK | GAAVFDALESEPELIERQRLRLR-QQELRARYNLSQGGYEELERVVRLKPHKAG--VQ- |

| | |
|--------------|---|
| AthTb005e07 | SGSANASDPAWDFASALFFASTLITTVGYGTTPLTDAGKAFSIAFALLGVPTTMLLLTA |
| hTWIK-1 | SGNWN----WDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIYSVIGIPFTLLFLTA |
| mTRAAK | TNSSNHSS-AWNLGSAFFSGTIITTIGYGNIVLHTDAGRFLCIFYALVGIPLFGMILLAG |
| mTREK-1 | SNQVSH----WDLGSSFFFAGTVITTIIGFGNISPRTEGGKIFCITYALLGIPLFGFLLAG |
| Athual133f10 | TSMGR----WELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFFALVGIPLNLVVLNR |
| FthKa20g4 | TFN-N----WNWPNAMIFAATVITTIIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWISA |
| hTASK | -----WRFAGSFYFAITVITTIIGYGHAASTDGGKVFCMFYALLGIPLTLVMFQS |

| | |
|--------------|---|
| AthTb005e07 | SAQLSLLLTH--VPLSWLSMRWGWDPRRAACWHLVALLGVVTVCFLVPAVIFAHLEEA |
| hTWIK-1 | VVQRITVHCTR--RPVLVFHWRGFSKQVVAIVHAVLLGFVTVSCKFFIPAAVFSVLEDD |
| mTRAAK | VGDRLLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLLFVLTPTFVFSYMES- |
| mTREK-1 | VGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFIILFGCVLFVALPAVIFKHIEG- |
| Athual133f10 | LGHLMQQGVNH---WASRLGGTWQD-PDKARWLAGSGALLSGLLLFLLLPPLLFSHMEG- |
| FthKa20g4 | LGKFFFGRAKR---LGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPVFMVTEG- |
| hTASK | LGERINTLVRY---LLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAFSHYEH- |

| | |
|--------------|--|
| AthTb005e07 | QTFRHVSSDLHGLTELILLPPP----- |
| hTWIK-1 | ETFCCELHELKKFRKMFYVKKDK----- |
| mTRAAK | NWLRAVSRRTRAEMGGLTAQAA----- |
| mTREK-1 | DWLRVISKKTKEEVGEFRAAAR----- |
| Athual133f10 | SQLETPGRVCSCCHSSKEDFK----- |
| FthKa20g4 | SMFVEVHKAIIKKRRRRKESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEETYNDLIK |
| hTASK | LRFMTMNAEDEKRDAEHRLALLTRN----- |

Fig. 7

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DV1M
Sheet 10 of 26

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| | | |
|-------------|---|---|
| AthTb005e07 | ----- | CPASFNADEDDRV----- |
| hTWIK-1 | ----- | DEDQVHIEHDQLSFSSIT----- |
| mTRAAK | ----- | SWTGTVTARVTQR-----T----- |
| mTREK-1 | ----- | EWTANVTAEFKETR-----R----- |
| Athua133f10 | ----- | SQSWRQGPDRPES-----HS----- |
| FthKa20g4 | ----- | QIGKKAMKTSGGGETGPGPGLPQGGGLPALPPSLVPLVVYSKNRVPTELLEVSQTLRSKG |
| hTASK | ----- | GQAGGGGGGSAHTTDAS----- |
| | | |
| AthTb005e07 | -DILGPQPESHQQ-- | LSASSHTDYASIPR----- |
| hTWIK-1 | -DQAAGMKEDQKQNEPFVATQSSACVDGPANH----- | |
| mTRAAK | -GPSAPPKEQPLLPSLAPPAVVEPAGRPGSPA----- | PAEKVETPSPPATA-SALDYPSEN |
| mTREK-1 | -RLSVEIYDKFQR-- | ATSVKRKLSAELAGNHNQELETPCMRTCL----- |
| Athua133f10 | -PQQGCYPEGPMG-- | IIQHLEPSAHAAGCGKDS----- |
| FthKa20g4 | HVSRSRSPDEEAVARAPEDSSPAPEVFMNQLDRISSEECEPWAQDYHPLIFQ-DASITFVNNT | |
| hTASK | -STAAAGGGGFRNVYAEVLHFQSMCSCLYWKSREKLQYSIPMIIPRDLSTS DTCVEQSHS | |
| | | |
| AthTb005e07 | ----- | ----- |
| hTWIK-1 | ----- | LAFIDESSDTQS ERG CALPRA P RGR RPNPSKKPSR PRGP GRL RD KAVPV----- |
| mTRAAK | ----- | |
| mTREK-1 | ----- | |
| Athua133f10 | ----- | |
| FthKa20g4 | EAGLSDEETS KSS LEDNLAGEESPQQGA EAKAPLN MGEFPSSSE STFTSTESEL SV PYEQ | |
| hTASK | SPGGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV----- | |
| | | |
| AthTb005e07 | ----- | ----- |
| hTWIK-1 | ----- | |
| mTRAAK | ----- | |
| mTREK-1 | ----- | |
| Athua133f10 | ----- | |
| FthKa20g4 | LMNEYNKANS PKGT | |
| hTASK | ----- | |

Fig. 7 (continued)

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DV1M

11/26

Clustal W (1.74) multiple sequence alignment

Fig. 8

Clustal w (1.74) multiple sequence alignment

TM 1

Athua133f10 -MYPRARAAPGRVRCAVPGTVLLLAYLAYLALGTGVFWTLLEGRAAQDSSRSFQRDK
 h TASK2 -----MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQK
 hTWIK-1 MLQSLAGSSCVRLVERHRSAWCFGFLVLYLVFGAVVSSVELPYEDLLRQELRKLK
 hTASK -----MKRQNVRTLALIVCTFTYLLVGAASFDALESEPE-LIERQRLELR
 * : ** .*: : * : * P-LOOP 1 : :

 Athua133f10 WELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTTSMGRWEVGSSFFSVSTITTIGY
 h TASK2 LHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQTFNN-WNWPNAMEFAATVITTIGY
 hTWIK-1 RRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY
 hTASK QQELRARYNLSQGGYEELERVVLRLKPH---KAGVQ---WRFAGSFYFAITVITTIGY
 . *. *.. :: : * TM 2 . * . :: * : : : : * **

 Athua133f10 GNLSPTMAARLFCIFFALVGIPPLNLVVLNRLGHLMQQGVNH--WASRLGGTWQDPDKAR
 h TASK2 GNVAPKTPAGRLFCVFYGLFGVPLCLTWISALGKFFGGRAKR--LGQFLTKRGVSLRKAQ
 hTWIK-1 GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVA
 hTASK GHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRV-LLHRAKKGLGMRRADVS
 * : * : .. * : * : * : * : TM 3 : : P-LOOP 2 : :

 Athua133f10 WLAGSGALLSGLLLFLPPPLFSHMEG-WSYTEGFYFAFITLSTVGFHDYVIG-MNPSQ
 h TASK2 ITCTVIFIVWGVVLVHLVIPIPFVFMVTEG-WNYIEGLYSFITISTIGFGDFVAG-VNPSA
 hTWIK-1 IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPG-EGYNQ
 hTASK MANMVLIGFFSCISTLCIGAAAFSHYEH-WTFFQAYYCFITLTITIGFDYVALQKDQAL
 . * : : * * : * : * : * : * : TM 4 : :

 Athua133f10 RYPLWYKNMVSLSWILFGMAWLALIKLILSQLETPGRVCSCCHSSKEDFKS-----
 h TASK2 NYHALYRYFVELWIYLGLAWLSLFVNWKVSMFVEVHKAIIKKRRRRKESFESSPHSRKAL
 hTWIK-1 KFRELYKIGITYCYLLLGLIAM-LVVLETFCHELKKFRKMFYVKKDKDEDQ-----
 hTASK QTTPQYVAFSFVYILTGLTVIGAFLNLVVLRFMTMNAEDEKRDAEHRALLTRNG-----
 . * : : * : : : : : :

 Athua133f10 QSWRQGPDRREPESHSPQQGCYPEG
 h TASK2 QVKGSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLGPQGGGLPAL
 hTWIK-1 -----VHIEHDQLSFSSITDQAAGMKED
 hTASK Q-----AGGGGGGGSAHTTDASSTAAAGGGG

 Athua133f10 PMGIIQHLEPSAHAAGCGKDS-----
 h TASK2 PPSLVPLVVYSKNRVPTELLEVSQTLRSKGHSVSRSPDEEAVARAPEDSSPAPEVFMNQLDR
 hTWIK-1 QKQNEPFVATQSSACVDGPANH-----
 hTASK FRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTS DTCVEQSHSSPGGGGRYSD
 :

 Athua133f10 ISEECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQQGAEAKA
 h TASK2 -----TPSRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV-----

 Athua133f10 PLNMGEFPSSSESTFTSTESELSVPYEQLMNEYNKANSPKG
 h TASK2 -----

Fig. 9

Applicants: Curtis, Rory A. J.
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GAP of: twik2.pep check: 1565 from: 1 to: 499

TWIK2 FthKa20g4

to: twik3.pep check: 8445 from: 1 to: 332

TWIK3 Athual133f10 - jthual133f10, 1575 bases, 18 checksum.

Symbol comparison table:
/usr/local/gcg_9.1/gcgcrcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 396 Length: 517
Ratio: 1.193 Gaps: 3

Percent Similarity: 40.764 Percent Identity: 32.166

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

twik2.pep x twik3.pep

| | | | |
|-----|--|-----------------------------------|----|
| 1 | | MVDRGPLLTSAILFYLAIGAAIFEVLEEPHWKE | 33 |
| 1 | MYRPRARAAPEGRVRGCAVPGTVLLLAYLAYLALGTGVFWTLLEGRAAQD | 50 | |
| 34 | AKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQT.FNN | 82 | |
| 51 | SSRSFQRDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTTSMGR | 100 | |
| 83 | WNWPNAIMFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWISA | 132 | |
| 101 | WELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFFALVGIPNLNVVLNR | 150 | |
| 133 | LGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPVF | 182 | |
| 151 | LGHLMQQGVNHAWASRLGGTWQDPDKARLAGSGALLSGLLLFLPPPLL | 200 | |
| 183 | MVTEGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIY | 232 | |
| 201 | SHMEGWSYTEGFYFAFITLSTVGFVDYVIGMNPSQRYPLWYKNMVSLWIL | 250 | |
| 233 | LGLAWLSLFVNWKVSMFVEVKAIKKRRRRKESFESSPHSRKALQVKGS | 282 | |
| 251 | FGMAWLALIIKLILSQLETPGRVCSCCHHSSKEDFKSQSW.RQGPDRPE | 299 | |
| 283 | TASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLGPQGG | 332 | |
| 300 | SHSPQQGCY.....PEGPMGIIQHLEPSAHAAGCGKDS..... | 332 | |

Fig. 10

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DV1M
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GAP of: twik4.pep check: 9188 from: 1 to: 313

TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

to: twik2.pep check: 1565 from: 1 to: 499

TWIK2 FthKa20g4

Symbol comparison table:

/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 221 Length: 512
Ratio: 0.706 Gaps: 5
Percent Similarity: 37.667 Percent Identity: 27.333

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

twik4.pep x twik2.pep..

1 .MRRGALLAGALAAYAAYLVLGALLVARLEGPHEARLRAELETLRAQLLQ 49
.||| | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||. 1 MVDRGPPLTSAI...IFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLK 47
50 RSPCVAAPALDAFVERVLAAGRLGRVVLANASGSANASDPAWDFASALFF 99
|||. ||| . ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| 48 EFPCLGQEGLDKILEVVSDAACQGVAITGNQTFN.....NWNWPNAIMF 91
100 ASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTMLLLTAQAQLSLLL 149
||.||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| 92 AATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWISALGKFFGGRA 141
150 THVPLSWLSMRWGWDPRRAACWHLVALLGVVVTCFLPAPVIFAHLEEAW 199
||.||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| 142 KR..LGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFM.VTEGW 188
200 SFLDAFYFCFISLSTIGLDYVPGEAPGQPYRALYKVLVTVYLFLGLVAM 249
||.||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| 189 NYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGL.AW 237
250 VLVLQTFRHVSDLHGLTELILLPPPCPASNADDEDRVDIRLGPQPEHQ 299
||.||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| 238 LSLFVNWKVSMFVEVHKAIKKRRRRKESFESSPHSRKALQVKGSTASKD 287
300 LSASSHTDYASIPR..... 313
288 VNIFSFLSKKEETYNDLIKQIGKKAMKTSGGETGPGPGLGPQGGGLPAL 337

Fig. 11

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DV1M

15/26

GAP of: twik3.pep check: 8445 from: 1 to: 332

TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.

to: twik4.pep check: 9188 from: 1 to: 313

TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

```
Symbol comparison table:  
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 6430
```

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 257 Length: 345
Ratio: 0.821 Gaps: 7
Percent Similarity: 40.333 Percent Identity: 31.667

Match display thresholds for the alignment(s):

! = IDENTITY
: = 2
. = 1

twik3.pep x twik4.pep...

Fig. 12

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DVIM

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GAP of: htwik-1.pep ch ck: 4093 from: 1 to: 336

hTWIK-1 U33632 Human two P-domain K⁺ channel TWIK-1 mRNA, complete cds.

to: twik2.pep check: 1565 from: 1 to: 499

TWIK2 FthKa20g4

Symbol comparison table:

/usr/local/gcg_9.1/gcgcrcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 269 Length: 521
Ratio: 0.801 Gaps: 4
Percent Similarity: 36.943 Percent Identity: 26.433

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

htwik-1.pep x twik2.pep

| | | |
|-----|---|-----|
| 1 | MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELPYED | 50 |
| 1 |MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWK | 32 |
| 51 | LLRQELRKLIKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW | 100 |
| 33 | EAKKNYYTQQLHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQTFN. | 81 |
| 101 | NWDFTSALFFASTVLSTTGYGHGVPLSDGGKAFCIYSVIGIPFTLLFLT | 150 |
| 82 | NWNWPNAMEFAATVITTIYGIVNVAPKTPAGRLFCVFYGLFGVPLCLTWIS | 131 |
| 151 | AVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIPA | 200 |
| 132 | ALGKFFGGRAKR..LGQFLTKRGVSLRKAQITCTVIFIVVGVLVHLVIPP | 179 |
| 201 | AVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEYNQKFRELYKIGIT | 250 |
| 180 | FVFMVTE.GWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVE | 228 |
| 251 | CYLLLGL..IAMLVVLETFCHELKKFRKMFYVKKDKDEDQVHIIEHDO | 298 |
| 229 | LWIYLGLAWLSLFVNWKVSMFVEVHKAIKKRRRRKESFESSPHSRKALQ | 278 |
| 299 | LSFSSITDQAAGMKEDQKQNEPFVATQSSACVDGPANH..... | 336 |
| 279 | VKGSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLG | 328 |

Fig. 13

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DV1M

17/26

GAP of: htwik-1.pep check: 4093 from: 1 to: 336

hTWIK-1 U33632 Human two P-domain K⁺ channel TWIK-1 mRNA, complete cds.

to: twik3.pep check: 8445 from: 1 to: 332

TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.

Symbol comparison table:

/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 199 **Length:** 337
Ratio: 0.599 **Gaps:** 3

Percent Similarity: 31.420 Percent Identity: 22.961

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

htwik-1.pep x twik3.pep...

1 MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLLVFGAVVFSSVELPYED 50
1 : . . | . | . | . | | | | | | | .. |
1 . MYRPRARAAPEGRVRGCAVPGTVL LLLAYLAYLA LGTGVFWTL EGRAAO 49

51 LLRQELRKLRKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW 100

50 DSSRSFORDKWELLONETCLDRPALDSLIRDVVOAYKNGASLLSNTTSMG 99

101 NWDETSALLEFASTVLSSTTGYHTVPLSDGGKAFCILLYSVIGIPETLLELT 150

100 RWEILVGSEEEFESVSTTTTIGYGNISPNNTMAARIECIEFAALVGIPNLIVVVLN 149

151 AYVORITYHVTBRRPVLYEHTRWGESKOVVATYHAVILLGEVTVSCEEEITPA 200

151 KVVKRITVAVTAKI VELPHKRGPSKQVVAIVAEVGGVVSCFVPA 200
152 RICHLIMOCGYNHWAISRLGCCTWODPRDKARWLACSCALLSCILL ELLIPB 187

201. NYESÜL EREDVÉNEI LÉSEGECELSÍ STÍLUSOK BEMUTATÁSA 350

201 AVFSVLEDDWNFLESPIFCFISLSITIGLGDIIVPGEGIYNQRFRELIRIGT 250

251 GYUUGLGLMVELE TEGIYVLLKPPRPTTQWVDPDQWLTQWQI 260

251 CYLLGLTAMLVLE.TFCELHELKKFRKMFYVKRDKRDEDQVH1IEHDQL 299

247 LWILFGMAWLALIIRLILSQLETPGRVCSCCHSSKEDFKS

300 SFSSITDOAAGMKEDOKONEPFVATOSACVDGPANH 336

297 EPESHSP00GCPYEGPMGIIOHLEPSAHAAGCGKDS. 332

Digitized by srujanika@gmail.com

Fig. 14

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray .
Docket No.: MPI99-025CP2DV1M

18/06

18726

GAP of: htwik-1.pep check: 4093 from: 1 to: 336

hTWIK-1 U33632 Human two P-domain K⁺ channel TWIK-1 mRNA, complete cds.

to: twik4.pep check: 9188 from: 1 to: 313

TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

Symbol comparison table:

/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 575 **Length:** 353
Ratio: 1.837 **Gaps:** 4

Percent Similarity: 55.405 Percent Identity: 46.284

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

htwik-1.pep x twik4.pep..

| | | |
|-----|--|-----|
| 1 | MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELPYED | 50 |
| 1 |MRRGALLAGALA.AYAAYLVLGALLVARLEGPHEA | 34 |
| 51 | LLRQELRKLRKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW | 100 |
| 35 | RLRAELETLRAQQLQRSPCPVAAPALDAFVERVLAAGRLGRVVLANASGSA | 84 |
| 101 | N.....WDFTSALFFASTVLSSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT | 145 |
| 85 | NASDPAWDFASALFFASTLITVGYGYTTPLTDAGKAFSIAFALLGVPTT | 134 |
| 146 | LLFLTAVVQRITVHVTRRPVLYFHIRWGFSKVVAIVHAVLLGFVTVSCF | 195 |
| 135 | :MLLTASAQRLSLLLTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCA | 184 |
| 196 | FFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLDYVPGEGYNQKFRELY | 245 |
| 185 | FLVPAVIFAHLEEAWSFLDAFYFCFISLSTIGLDYVPGEAPGQPYRALY | 234 |
| 246 | KIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVK.....KDKDE | 288 |
| 235 |KVLVTVYLFLGLVAMVLVLQTFRHVSIDLHGLTELILLPPPCPASFNADED | 284 |
| 289 | DQVHII.....EHDQLSFSSITDQAAGMKEDQKQNEPFVATQSSACVDGP | 333 |
| 285 |DRVDIRGPQPESHQQLSASSHTDYASIPR..... | 313 |

Fig. 15

Applicants: Curtis, Rory A. J.
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GAP of: htask2.pep check: 1565 from: 1 to: 499

hTASK2 3925427 in GenPept

to: twik2.pep check: 1565 from: 1 to: 499

TWIK2 FthKa20g4

Symbol comparison table:

/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 2613 Length: 499

Ratio: 5.236 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

htask2.pep x twik2.pep..

| | | |
|-----|---|-----|
| 1 | MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFP | 50 |
| 1 | MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFP | 50 |
| 51 | CLGQEGLDKILEVVSDAAGQGVAITGNQTFNNWNWPNAMIFAATVITIIG | 100 |
| 51 | CLGQEGLDKILEVVSDAAGQGVAITGNQTFNNWNWPNAMIFAATVITIIG | 100 |
| 101 | YGNVAPKTPAGRFLFCVFYGLFGVPLCLTWISALGKFFGGRAKRLGQFLTK | 150 |
| 101 | YGNVAPKTPAGRFLFCVFYGLFGVPLCLTWISALGKFFGGRAKRLGQFLTK | 150 |
| 151 | RGVSLRKAQITCTVIFIVWGVLVHLVIPPVFMTEGWNYIEGLYYSFIT | 200 |
| 151 | RGVSLRKAQITCTVIFIVWGVLVHLVIPPVFMTEGWNYIEGLYYSFIT | 200 |
| 201 | ISTIGFGDFVAGVNP SANYHALYRYFVELWIYLGLAWLSLFVNWKVSMFV | 250 |
| 201 | ISTIGFGDFVAGVNP SANYHALYRYFVELWIYLGLAWLSLFVNWKVSMFV | 250 |
| 251 | EVHKAIKKRRRRKESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEET | 300 |
| 251 | EVHKAIKKRRRRKESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEET | 300 |
| 301 | YNDLIKQIGKKAMKTSGGGETGPGPGLPQGGGLPALPPSLVPLVVYSKN | 350 |
| 301 | YNDLIKQIGKKAMKTSGGGETGPGPGLPQGGGLPALPPSLVPLVVYSKN | 350 |

Fig. 16

351 RVPTLEEVSQTLRSKGHVSRS PDEEAVARAPEDSSPAPEVFMNQLDRISE 400
351 RVPTLEEVSQTLRSKGHVSRS PDEEAVARAPEDSSPAPEVFMNQLDRISE 400
401 ECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQ 450
401 ECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQ 450
451 QGAEAKAPLNMGEPSSSESTFTSTESELSPVYEQLMNEYNKANSPKGT 499
451 QGAEAKAPLNMGEPSSSESTFTSTESELSPVYEQLMNEYNKANSPKGT 499

Fig. 16 (continued)

>human TWIK 5

CTAGGGAGGGCGCCATCTGAGTAGTCGGAAGAACTGAACATGATGAGTT
GCCGGCTGCTTCCTGAGTCCTGGGAAGCACACGCACCATCCACTTAGC
ACTGGAGCCTGGCTGTTCTCCGGGACTCCTACCCATCTCCTGGCGGG
GCTTAGATGCTCCTGCCCTTCCACCAAGCTCCTTGCCCTGCATGCTTC
AGGGACGATGGAGGTCTCGGGGACCCCCAGGCCAGGAGATGCTGCCAG
AGGCCCTGGGAAAGCTTCCCTGGCCTTGCTTCCTGCTTCTGGTG
ACCTACGCCCTGGTGGGTGCTGTTCTGCCCATTGAGGACGGCCA
GGTCCTGGTGGCAGCAGATGATGGAGAGTTGAGAAGTTCTGGAGGAGC
TCTGCAGAACATTTGAACTGCAGTGAAACAGTGGTGGAAAGACAGAAAACAG
GATCTCCAGGGCATCTGCAGAAGGTGAAGCCTCAGTGGTTAACAGGAC
CACACACTGGCCTTCTGAGCTCGCTTTCTGCTGCACGGTGTCA
GCACCGTGGCTATGGCTACATCTACCCGTCACCAGGCTGGCAAGTAC
TTGTGCATGCTCTATGCTCTTGGTATCCCCGTGATGTTCTCGTTCT
CACGGACACAGGCACATCCTGGCAACCATCTATCTACATCTTATAATC
GGTCCGAAAATCCCTTCTTACCCGCCCCCTCCTCCAAGTGGTGC
CCCAAATCTCTTCAAGAAAAACGGACCCCAAGCCGCAGATGAAGC
TGTCCCTCAGATCATCATCAGTGTGAAGAGCTCCAGGCCAAACTG
GCACATGTCCTTCACGCCAAGCTGCAGCATGGAGCTGTTGAGAGATCT
CATGCGCTAGAGAACAGAACACACTGCAACTGCCCAAGCCATGGA
GAGGAGTAACCGTGTCCCAGACTGGTGGAGACAGTGGATTCGAGAATGCCTTCT
TCATCAGCAACCTGGATGAAGTGGACAGCAGGTGGAGAGGTTGGACATC
CCCCTCCCCATCATTGCCCTTATTGTTTGCTACATTTCTGTGCAGC
TGCCATCCTCCCTTCTGGAGACACAGTGGATTCGAGAATGCCTTCT
ATTTCTGCTTGTCAACTCACCACATTGGGTTGGGATACTGTTTA
GAACACCCTAACCTCTCCTGTTCTCCATTATATCATCGTTGGAAT
GGAGATTGTGTTCATGCTTCAAGTGGTGCACAGGCTGATTGACA
TATAACAAAATGTTATGCTATTGCAAAAGGGAAGTTTACCAACCTT
GTTAAAAGTGAAGGTTCAATTCTCAGGTGACAGACACTGGCTGAG
CTGGTTTCTGTGTTCTCAGGGTCACTGCAGCCTGTCACCTGAGAC
CTTCAGTCTGGAGACAAATCCCTATGAGAGCCAAGTCAGTCTTGAGG
CCCTGC

MLLPLPPAPLALHASGTMEVSGHPQARRCCPEALGKLFPGLCFLCFLVTYALVGAVV
FSAIEDGQVLVAADDGEFEKFLEELCRILNCSETVVEDRKQDLQGHLQKVKPQWFNR
TTHWSFLSSLFFCCTVFSTVGYGYIYPVTRLGKYLMLYALFGIPLMFLVLTDTGDI
LATILSTSYNRFRKFPFFTRPLLSWCPKSLFKKPDPKPADEAVPQIIISAEELPG
PKLGTCP SRPSCSMELFERSHALEKQNTLQLPPQAMERSNSCPELVLGRLSYSIIISN
LDEVGQQVERLDIPLPIIALIVFAYISCAAAILPFWETQLDFENAFYFCVTLTTIG
FGDTVLEHPNFFLFFSIYIIVGMEIVFIAFKLVQNRLIDYKNVMLFFAKGKFYHLV
KK

Fig. 17

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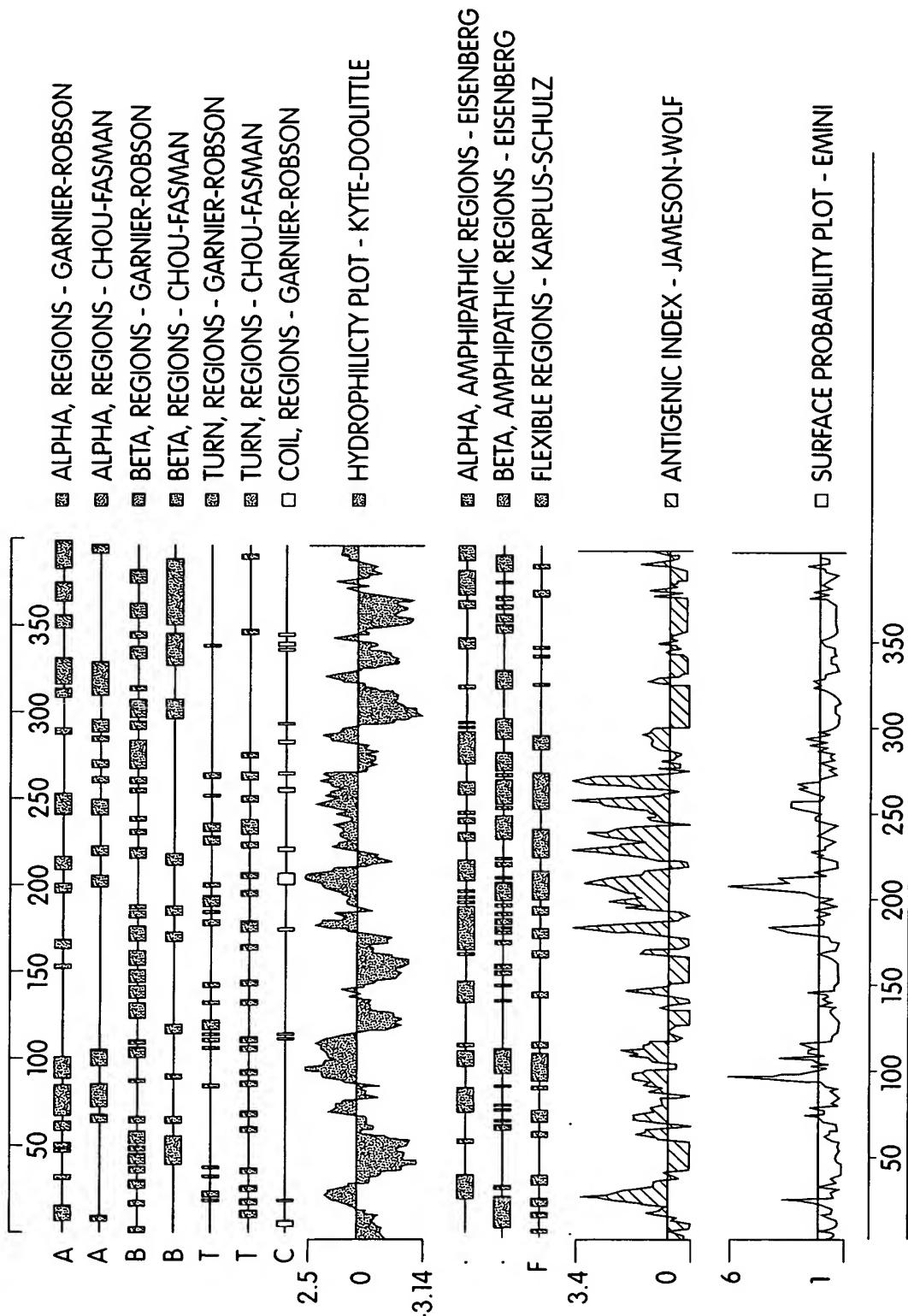


Fig. 18

23/26

GAP of: ORBa005gy ch ck: 9848 from: 1 to: 401

TWIK-5 protein (analysis onl - Import - compl t

to: PRBa005gy check: 4672 from: 1 to: 394

2465542 in GenPept

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/PAM250
CompCheck: 5553

Gap Weight: 25 Average Match: 2.617
Length Weight: 1 Average Mismatch: -3.416

Quality: 166 Length: 538
Ratio: 0.421 Gaps: 5
Percent Similarity: 49.805 Percent Identity: 29.183

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

ORBa005gy x PRBa005gy

| | | | |
|-----|---|---------------------|-----|
| 1 | MLLPLPPAPLALHASGTMEVSGHPQARRCCPEALGKLFPGLCFLCFLVTY | 50 | |
| 1 | | MKRQNVRRTLALIVCTFTY | 18 |
| 51 | ALVGAVVFSAIEDGQVLVAADDGEFEKFLEELCRILNCSETVVEDRKQDL | 100 | |
| 19 | LLVGAASFDALESEPELIERQRLELRQ | 62 | |
| 101 | QGHLQKVKPQWFNRTTHWSFLSSLFFCCTVFSTVGYGYIYPVTRLGKYLC | 150 | |
| 63 | ERVVRLKPH..KAGVQWRFAGSFYFAITVITTIGYHAAPSTDGGKVFC | 110 | |
| 151 | MLYALFGIPLMFLVLTDTGDILATILSTSYNRFRKFPFFTRPLLSKWCPK | 200 | |
| 111 | MFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKK | 145 | |
| | . | | |
| | . | | |
| 251 | LEKQNTLQLPPQAMERSNSCPELVLGRLSYSIIISNLDEVGQQVERLDIPL | 300 | |
| 146 | | GLGMRRADVSM | 156 |
| 301 | PIIALIVF..AYISCAAAILPFWETQLDFENAFYFCFVTLTTIGFD.. | 345 | |
| 157 | ANMVLIGFFSCISTLCIGAAAFSHYEHWTFQAYYYCFITLTTIGFDYV | 206 | |
| 346 |TVLEHPNFFLFFSIYIIVGMEIVFIAFKLVQNRIDIVKNVMLF | 389 | |
| 207 | ALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVVLRFMTMNAEDEKR | 256 | |
| 390 | FAKGKFYHLVKK | 401 | |
| 257 | DAEHALLTRNGQAGGGGGGSAHTTDASSTAAAGGGFRNVYAEVLHF | 306 | |

Fig. 19

Applicants: Curtis, Rory A. J.
Title: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI99-025CP2DV IM
Sheet 24 of 26

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GAP of: GRBa005gy ch ck: 9848 from: 1 to: 401
TWIK-5 prot in (analysis onl - Import - complet
to: HRBa005gy check: 2856 from: 1 to: 426
4101566 in GenPept

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/PAM250
CompCheck: 5553

| | | | |
|---------------------|--------|-------------------|--------|
| Gap Weight: | 25 | Average Match: | 2.617 |
| Length Weight: | 1 | Average Mismatch: | -3.416 |
| Quality: | 77 | Length: | 563 |
| Ratio: | 0.192 | Gaps: | 6 |
| Percent Similarity: | 44.697 | Percent Identity: | 27.273 |

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

GRBa005gy x HRBa005gy

| | | | |
|-----|--|---------------------|-----|
| 1 | | MLLPLPPAPPLALHASGTM | 18 |
| 1 | MLPSASRERPGYRAGVAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVES | .. | 50 |
| 19 | EVSGHPQARRCCPEALGKLFPGLCFLCFLVTYALVGAVVFSAIEDGQVLV | .. | 68 |
| 51 | DTTINVMWKTVST.....IFLVVVLYLIIGATVFKALEQPHEIS | .. | 90 |
| 69 | AADDGEFEK..FLEELCRILNCSETVVEDRKQDLQGHLQKVKPQWFNRTT | .. | 116 |
| 91 | QRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNTSNQIS | .. | 140 |
| 117 | HWSFLSSLFFCCTVFSTVGYYIYPVTRLGKYLCMLYALFGIPLMFLVLT | .. | 166 |
| 141 | HWDLGSSFFFAGTVITTIIGGNISPRTEGGKIFCIYALLGIPFGFLLA | .. | 190 |
| 167 | DTGDILATILSTSYNRFRKFPPTRPLLSKWCPSLFFFPADEAV | .. | 216 |
| 191 | GVGDQLGTIFGKG..... | .. | 203 |
| | | .. | |
| 267 | SNSCPELVLGRLSYSIISNLDEVGQQVERLDIPLPIIALIVFAYISCA.. | .. | 314 |
| 204 | IAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLF | .. | 237 |
| 315 | ...AAILPFWETQLDFENAFYFCFVTLLTIGFGDTVLEHPNFFLFFSIYI | .. | 361 |
| 238 | VALPAIIFKHIEGWSALDAIYFVVITLTTIGFGD.....YV | .. | 273 |
| 362 | IVGMEIVFIAFKLVQNRLIDIIYKNVMLFFAKGKFYHLVKK..... | .. | 401 |
| 274 | AGGSDIEYLD.....YKPVVWFWILVGLAYFAAVLSMIGRLVRV | .. | 313 |
| | | .. | |

Fig. 20

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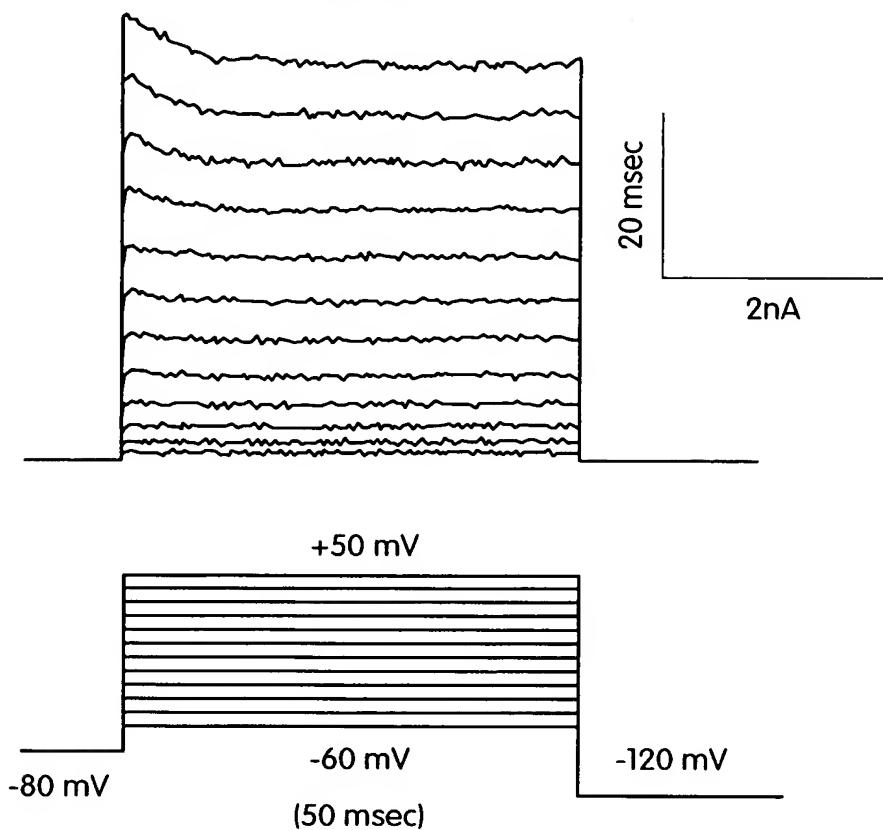


Fig. 21A

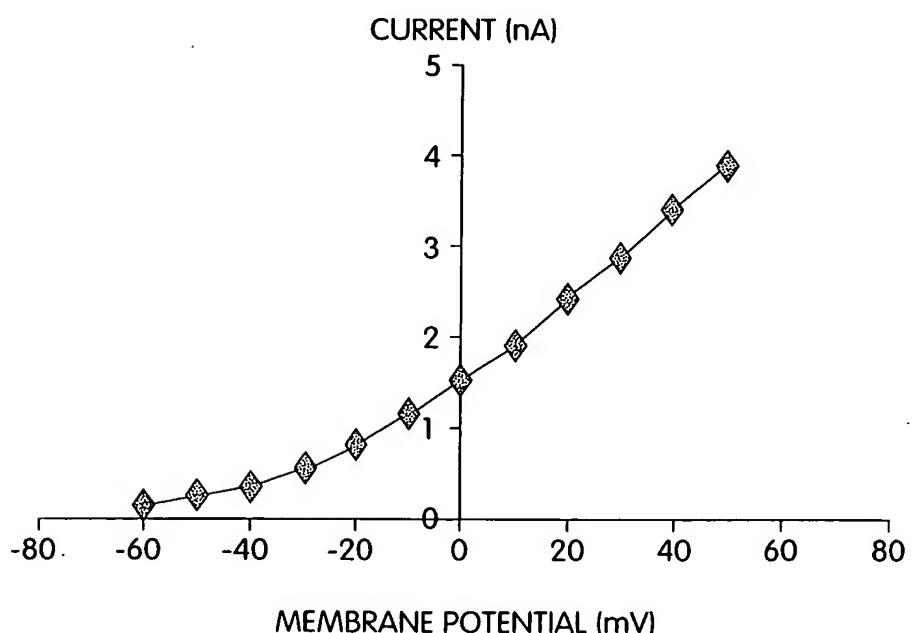


Fig. 21B

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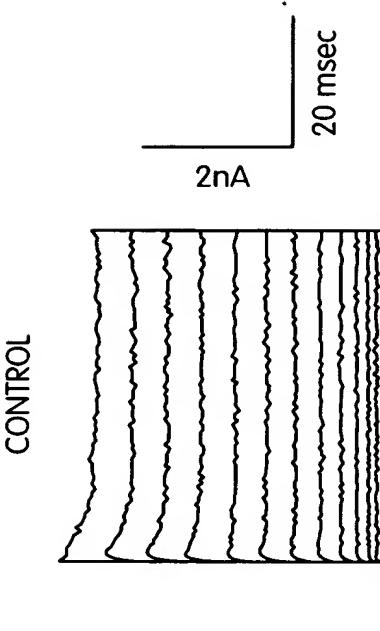


Fig. 22A

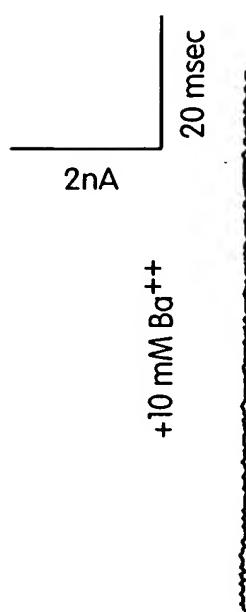


Fig. 22B

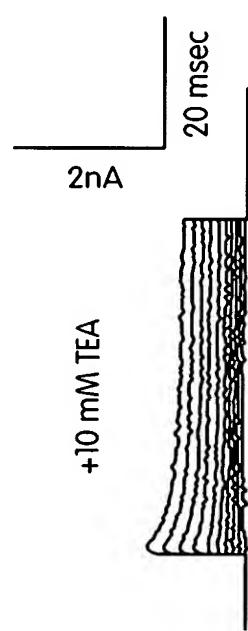


Fig. 22C

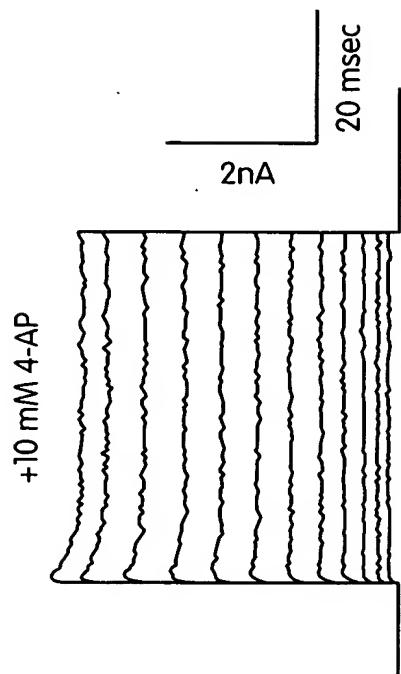


Fig. 22D